

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: DAUGHERTY, BRUCE L.
DEMARTINO, JULIE A.
SICILIANO, SALVATORE J.
SPRINGER, MARTIN J.
- (ii) TITLE OF THE INVENTION: EOSINOPHIL EOTAXIN RECEPT
OR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Merck & Co., Inc.
(B) STREET: P.O. Box 2000, 126 E. Lincoln Ave.
(C) CITY: Rahway
(D) STATE: NJ
(E) COUNTRY: USA
(F) ZIP: 07065-0900
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/847,296
(B) FILING DATE: 24-APR-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/016,158
(B) FILING DATE: 26-APR-1996

(A) APPLICATION NUMBER: 60/017,113
(B) FILING DATE: 26-APR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Thies, J. Eric
(B) REGISTRATION NUMBER: 35,382
(C) REFERENCE/DOCKET NUMBER: 19634Y
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 908-594-3904
(B) TELEFAX: 908-594-4720
(C) TELEX:



(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Thr	Thr	Ser	Leu	Asp	Thr	Val	Glu	Thr	Phe	Gly	Thr	Thr	Ser	Tyr	1	5	10	15
Tyr	Asp	Asp	Val	Gly	Leu	Leu	Cys	Glu	Lys	Ala	Asp	Thr	Arg	Ala	Leu	20	25	30	
Met	Ala	Gln	Phe	Val	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Thr	Val	Gly	35	40	45	
Leu	Leu	Gly	Asn	Val	Val	Val	Val	Met	Ile	Leu	Ile	Lys	Tyr	Arg	Arg	50	55	60	
Leu	Arg	Ile	Met	Thr	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	65	70	75	80
Leu	Leu	Phe	Leu	Val	Thr	Leu	Pro	Phe	Trp	Ile	His	Tyr	Val	Arg	Gly	85	90	95	
His	Asn	Trp	Val	Phe	Gly	His	Gly	Met	Cys	Lys	Leu	Leu	Ser	Gly	Phe	100	105	110	
Tyr	His	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	115	120	125	
Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala	130	135	140	
Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Val	Thr	Trp	Gly	Leu	145	150	155	160
Ala	Val	Leu	Ala	Ala	Leu	Pro	Glu	Phe	Ile	Phe	Tyr	Glu	Thr	Glu	Glu	165	170	175	
Leu	Phe	Glu	Glu	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Pro	Glu	Asp	Thr	Val	180	185	190	
Tyr	Ser	Trp	Arg	His	Phe	His	Thr	Leu	Arg	Met	Thr	Ile	Phe	Cys	Leu	195	200	205	
Val	Leu	Pro	Leu	Leu	Val	Met	Ala	Ile	Cys	Tyr	Thr	Gly	Ile	Ile	Lys	210	215	220	
Thr	Leu	Leu	Arg	Cys	Pro	Ser	Lys	Lys	Lys	Tyr	Lys	Ala	Ile	Arg	Leu	225	230	235	240
Ile	Phe	Val	Ile	Met	Ala	Val	Phe	Phe	Ile	Phe	Trp	Thr	Pro	Tyr	Asn	245	250	255	
Val	Ala	Ile	Leu	Leu	Ser	Ser	Tyr	Gln	Ser	Ile	Leu	Phe	Gly	Asn	Asp	260	265	270	
Cys	Glu	Arg	Ser	Lys	His	Leu	Asp	Leu	Val	Met	Leu	Val	Thr	Glu	Val	275	280	285	
Ile	Ala	Tyr	Ser	His	Cys	Cys	Met	Asn	Pro	Val	Ile	Tyr	Ala	Phe	Val	290	295	300	
Gly	Glu	Arg	Phe	Arg	Lys	Tyr	Leu	Arg	His	Phe	Phe	His	Arg	His	Leu				

305		310		315		320									
Leu	Met	His	Leu	Gly	Arg	Tyr	Ile	Pro	Phe	Leu	Pro	Ser	Glu	Lys	Leu
			325						330					335	
Glu	Arg	Thr	Ser	Ser	Val	Ser	Pro	Ser	Thr	Ala	Glu	Pro	Glu	Leu	Ser
			340					345					350		
Ile	Val	Phe													
		355													

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ATGACAACCT CACTAGATAC AGTTGAGACC TTTGGTACCA CATCCTACTA TGATGACGTG
60
GGCCTGCTCT GTGAAAAGC TGATACCAGA GCACTGATGG CCCAGTTTGT GCGGCGCTG
120
TACTCCCTGG TGTTCACTGT GGGCCTCTTG GGCAATGTGG TGGTGGTGAT GATCCTCATA
180
AAATACAGGA GGCTCCGAAT TATGACCAAC ATCTACCTGC TCAACCTGGC CATTTCGGAC
240
CTGCTCTTCC TCGTCACCCT TCCATTCTGG ATCCACTATG TCAGGGGGCA TAACTGGGTT
300
TTTGCCCATG GCATGTGTAA GCTCCTCTCA GGGTTTATC ACACAGGCTT GTACAGCGAG
360
ATCTTTTCA TAATCCTGCT GACAATCGAC AGGTACCTGG CCATTGTCCA TGCTGTGTTT
420
GCCCTTCGAG CCCGGACTGT CACTTTTGGT GTCATCACCA GCATCGTCAC CTGGGGCCTG
480
GCAGTGCTAG CAGCTCTTCC TGAATTTATC TTCTATGAGA CTGAAGAGTT GTTTGAAGAG
540
ACTCTTTGCA GTGCTCTTTA CCCAGAGGAT ACAGTATATA GCTGGAGGCA TTTCCACACT
600
CTGAGAATGA CCATCTTCTG TCTCGTTCTC CCTCTGCTCG TTATGGCCAT CTGCTACACA
660
GGAATCATCA AAACGCTGCT GAGGTGCCCC AGTAAAAAAA AGTACAAGGC CATCCGGCTC
720
ATTTTGTGCA TCATGGCGGT GTTTTTCATT TTCTGGACAC CCTACAATGT GGCTATCCTT
780
CTCTCTTCCT ATCAATCCAT CTTATTTGGA AATGACTGTG AGCGGAGCAA GCATCTGGAC
840
CTGGTCATGC TGGTGACAGA GGTGATCGCC TACTCCCACT GCTGCATGAA CCCGGTGATC
900
TACGCCTTTG TTGGAGAGAG GTTCCGGAAG TACCTGCGCC ACTTCTTCCA CAGGCACTTG
960

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CTCATGCACC TGGGCAGATA CATCCCATTC CTCCTAGTG AGAAGCTGGA AAGAACCAGC
1020
TCTGTCTCTC CATCCACAGC AGAGCCGGAA CTCTCTATTG TGTTT
1065

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCCTAC CTTCCCCATC AGAGCTAGGG GGCATGGAGC GCTCTCTGCT AAGATGGGGA
60
CCCCCAAGGA ATGTCTCCCT GTGGGGCACT TCCTTACCAG ATGGGATGGC CAGTGCGGTT
120
AAGTTGGTGG TCAGGCAGAA AAAAAAGATC TAGTTTGTAC TCTTGAGAGT TCCTCGGTTT
180
GTTTCATGGCA TGGGCAGGGA GTCAAGGAGC AGCAGCCTTG CCTCAGTGCC TACCAGTGCA
240
GGAAAAGGTG CATAGCCTGG GCCAGGGCCA GGGCCCTGGT GGAGGCGTAG TGGTAACAGA
300
GAGGGCTCTC CATTCCAGCC CAAGGAAGAC TAAGAATGAA TACCTCATGA GTATATTAGC
360
TACAAACCAC CACAGCAGGT TCCAGAAAAA GGCTCAGCGT TGGAACCAGG TCACCCCCAC
420
TCAGCAGACA CCAGTCATAT AAATCAAGGA CCAACAGGAG ACAGGAACAC CCCCTTCCCA
480
CTCTGCCCCA TGTCTCAAGT TGTAGTGGCC CTCCTCCAG ATCTCTGCCA CCATCTTAGA
540
AAGGAACACT GAAAGAAGAA ACTGAAATTA TAAGCTGACA GCATAAAGAG GATGAGTAAA
600
ACCTAAAATC ATTGTTTACA TGAATGAATC AAGAGAAAGT TAAACCACTT TGGACTAAAA
660
TGTGTGAATC CTTTTTCCTG CTATCCAGCA GATGAGAAGC TGGTAACAGA GACCACAATA
720
GTTTGGAGAC TAAAGAATCA TTGCACATTT CACTGCTGAG TTGTATTGTG AGTAATTTTA
780
GTTGACCTCA CTTTGTAAT CTTGCACACG GGGCAATCCA ATATCTGCAC AAGAGATATG
840
TTAACCAGTG GTAAATGCTG CATGAGGAGA TTGGGTGATT TTTACTTTCG TTTTGTGCT
900
CTTCTTTCTT ATTGTTCTTA CTTATTTACG ATTACCCTAT CGTTTTCCCA AAATGTAAAA
960
GGCCATTTTG AAAGCCTAAT TCAAACCTCT TCACTATTTT GTATCTAAGT ATTCACCTTG
1020

ATTGAGACTG GGTAGACAGG TGAAAACCAT ATCAGGTTTT TAATTTTTTA ATTTTAAATT
1080
ATTTATTTAT TTATTTATTT TTTGAGATGG AGTCTGGCTG TCGCCCAGGC TGGAGTGCAG
1140
CGGCGTGATC ACAGTTCAC TGCAGCCTCAA CCTTCTAGGC TCAAGGGATT CTCCCACCTC
1200
AGCCCCCAA GTAGTTGGGA CCACACGTAT GCGCCACCAT GCCTGGCTAA TTTCTTATTT
1260
TTTTGTAGAG ATAGGATCTC ACTATATTGT CCAGGCTGGT CTTGAATTCC TGGGCTCAGG
1320
TGAGCCTCCC ACCTGGGCCT CCCAAAGTAC TGGGATTACA GGCATGAGCC AAGGTCCCTT
1380
GCCCCATATGA GATTTTCTGT CTCTGATCCC ATGCAGCTAG TAATCAAGGA CTTGGCTGCT
1440
GACTCTGGAG GACCTGCATG CTTTCTTGAG CTGTGAACTT CAGTGCTAAA AGCTCATAGG
1500
CAGCCCTGAA ACCCAAACCA AAAGGTCTA TGGTTTATCA TCCTGATCAT GTTGATTTTA
1560
TAGAAATAAC ACATGAATTA AAGACACTAC CCTCAAACCTG AGCAAACCTT AAGTAATTTT
1620
TTTAAAGTTT GACCTGTTTT TAAATCACTC TTGGAGAAAA AGGAAAATAA ATACAAATAA
1680
TTAACGGTGA ATACAGGCTA CTATACCTTT GTTCTCCAGA ATTAGCAGTT CTGTTCTTTT
1740
CTTGCTTTAG ATGCTGAAGT GCAGAAGGAC ACTCTGTGAT TGTACGTGTG TAACTGACAA
1800
AATGTGTATT TTTTCTCTCA GCTGCTATGG ATTGGATTAT GCTATTATGA ATAAGAATGC
1860
TGATGGGAGC ACACACAAAC CATTTGTTCC TCAGTCCATT TTCCTCCTCA AAAGCCTGGA
1920
ATGTGCCATT GATCAGTGGG AGATGTACCT GGACAGACCC ATGAAAAGAG ATCAACAAGT
1980
TCCACCCAAG GGACCCTATT TTTCCTAATT TCATTGAAA TGGCTTCTAA TTGTCCTTCT
2040
TTCATTCTG CTCCTACCA GTTTTACAGC TTTTCTGGT TTCAAATGTG AACTCACATA
2100
CACTCTCATT TTTCCTCATC ACAACCCCAA GTGACCCAAT GGTCTCACT TTCGATATAA
2160
GTAAAGGAGG CTCTGCATTA AGGGCTTGTC CAAGGCACGC AGCTGAGAGG CGCTAGGACT
2220
GGCTCCATTT CCATCTCTAT TCTCACTGAC TTTGACTACC CAGAACCCCA ACATGTGGGG
2280
CCTCAGTATT CGATCAATTA TTCTATTAAG AAGCAAAAAC AATTCCCCGC ATTGGCCCCA
2340
GTTATTAAGC ATTTCTCAGA TTTACCTTGA GAAATGCCCA TCGGCCTGTA TATTCACATC
2400
TTCACCCTTG TCCCTTCCTC CTAGAAAGGA GAAAGTCAGT TGGATGCCCT CTGAGGAAC T
2460
AGTGCATGGC TTAAGTGTCC TTCCATGACT CCTGCCTTAT CTGTTTTCTA TTTCTCTCT
2520
TTTCCACCGA AGTCTATAAT CTCAAGAAAA GCAGGCACTG GCCTTAGGGC TCCTGGCCTA
2580

AGAAATATCA AGTCCAGTGA GAAATCCCAT TGA CTGACCC CTCCTGCTTA CCCCTTTGTG
2640
ATGGAGAAGC TCCCAGGGGT TTGCTTTTTG CATGTTACCA GGCCTAACTC AGCATCACCA
2700
GGGGCAAGAA AAGGAAAGTA ACCTAACTA ATGCTGCTTA TAATTGTAAT TATTGTAATA
2760
GTTAATTACT GTGATTGTAC ATGTGTAACA GACAAAATGT GTATTTTTTTT CACAGCTGCT
2820
GTGGATTGGA TTATGCCATT TGAATAAGA ATGCTGTAA GAGCACACAA GCCAGGTTCC
2880
TCAAGTCCGT AGCAAATTTT TCAAAAGTTA AATTTAAAAA TCACTACATT TGAATCTAGT
2940
GACAGGAGAA ATGGACATGG ATAGAGACTA AAGATCTAGC CCAAATTTTA TATTTACTTG
3000
TTAGAGGATT TTGAACAAAT TACTAAATTT CTTCAAGGTT CAATTTCCCC ATTA ACTATA
3060
ATGAATGTCT CATCATTATG GGGCCCTGGA GAAGCATAAT TACTTGTAAT TGTAATAATC
3120
ATTGTTATTA TTATTATACA TATTTTGCTT TTAAATGGAT AAGGATTTTT AAGGTATATG
3180
TAAACTGTAA AACATAAAAT GCAAAATGCC GTAAGAGACA GTAGTAATAA TAATGATTAT
3240
TATATTGTTA TCATTATCTA GCCTGTTTTT TCCTGTTGTG TATTTCTTCC TTAAATGCT
3300
TACAGAAAATC TGTATCCCCA TTCTTCACCA CCACCCACAC ACATTTCTGC TTCTTTTCCC
3360
ATGCCGGTCA TGCTAACTTT GAAAGCTTCA GCTCTTTCCT TCCTCAATCC TTCTCCTGGC
3420
ACCTCTGATA TGCCTTTTGA AATTCATGTT AAAGAATCCC TAGGCTGCTA TCACATGTGG
3480
CATCTTTGTT GAGTACATGA ATAAATCAAC TGGTGTGTTT TACGAAGGAT GATTATGCTT
3540
CATTGTGGGA TTGTATTTTT CTTCTTCTAT CACAGGGAGA AGTGAA
3586

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAGGTCAGAT GCAGAAAATT GCCTAAAGAG GAAGGACCAA GGAGATGAAG CAAACACATT
60
AAGCCTTCCA CACTCACCTC TAAAACAGTC CTTCAAACCT CCAGTGCAAC ACTGAAGCTC
120

TTGAAGACAC TGAAATATAC ACACAGCAGT AGCAGTAGAT GCATGTACCC TAAGGTCATT
180
ACCACAGGCC AGGGGCTGGG CAGCGTACTC ATCATCAACC CTAAAAAGCA GAGCTTTGCT
240
TCTCTCTCTA AAATGAGTTA CCTACATTTT AATGCACCTG AATGTTAGAT AGTTACTATA
300
TGCCGCTACA AAAAGGTAAA ACTTTTTATA TTTTATACAT TAACTTCAGC CAGCTATTGA
360
TATAAATAAA ACATTTTCAC ACAATACAAT AAGTTAACTA TTTTATTTTC TAATGTGCCT
420
AGTTCTTTCC CTGCTTAATG AAAAGCTT
448